

SEQ ID NO:4

16	1292	37.5	2192	2	Q49LL5_AEDAE	Q49ll15 aedes aegyp	RL Biochim. Biophys. Acta 1490:163-169(2000).
17	1284	37.3	2249	1	DCR1_DROME	Q9vcu9 drosophila	RN [2]
18	1283	37.2	2280	2	Q29AU1_DROPS	Q29au1 drosophila	RP NUCLEOTIDE SEQUENCE [mRNA].
19	1151	33.4	1845	1	DCR1_CAEEL	P34529 caenorhabdi	RC TISSUE=Lung;
20	1106.5	32.1	1863	2	Q60MW6_CAEBR	Q60mw6 caenorhabdi	RA Provost P., Dishart D., Doucet D., Hermansson A., Frendewey D.,
21	902	26.2	2043	2	Q27IU2_DROME	Q27iu2 drosophila	RA Samuelsson B., Radmark O.;
22	896	26.0	2043	2	Q27IT7_DROSI	Q27it7 drosophila	RT "RNA binding and processing by recombinant human Dicer.";
23	894	25.9	2043	2	Q27IT4_DROSI	Q27it4 drosophila	RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
24	894	25.9	2043	2	Q27IT9_DROSI	Q27it9 drosophila	RN [3]
25	894	25.9	2043	2	Q27IT6_DROSI	Q27it6 drosophila	RP NUCLEOTIDE SEQUENCE [LARGE SCALE mRNA].
26	894	25.9	2043	2	Q27IT8_DROSI	Q27it8 drosophila	RC TISSUE=Brain;
27	894	25.9	2043	2	Q27IU7_DROME	Q27iu7 drosophila	RX MEDLINE=99246063; PubMed=10231032; DOI=10.1093/dnarecs/6.1.63;
28	894	25.9	2043	2	Q27IU0_DROSI	Q27iu0 drosophila	RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosewa M.,
29	894	25.9	2043	2	Q27IU5_DROME	Q27iu5 drosophila	RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
30	894	25.9	2043	2	Q27IU9_DROME	Q27iu9 drosophila	RT "Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
31	894	25.9	2043	2	Q27IU4_DROME	Q27iu4 drosophila	RL DNA Res. 6:63-70(1999).
32	894	25.9	2043	2	Q27IU8_DROME	Q27iu8 drosophila	RN [4]
33	893	25.9	2043	2	Q27IU3_DROME	Q27iu3 drosophila	RP SEQUENCE REVISION.
34	893	25.9	2043	2	Q27IT5_DROSI	Q27it5 drosophila	RX MEDLINE=22158633; PubMed=12168954; DOI=10.1093/dnarecs/9.3.39;
35	892	25.9	2043	2	Q27IU6_DROME	Q27iu6 drosophila	RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
36	888	25.8	2043	2	Q27IU1_DROSI	Q27iu1 drosophila	RT "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA cDNA clones.";
37	713	20.7	149	2	Q862N0_BOVIN	Q862n0 bos taurus	RL DNA Res. 9:99-106(2002).
38	631	18.3	1658	2	Q174T8_AEDAE	Q174t8 aedes aegyp	RN [5]
39	624	18.1	1715	2	Q29IA3_DROPS	Q29ia3 drosophila	RP NUCLEOTIDE SEQUENCE [mRNA] OF 1238-1912.
40	623	18.1	1658	2	Q49LL4_AEDAE	Q49ll14 aedes aegyp	RC TISSUE=Lung;
41	616.5	17.9	1719	2	Q2Q3U0_DROYA	Q2q3u0 drosophila	RX MEDLINE=99162526; PubMed=10051563; DOI=10.1073/pnas.96.5.1881;
42	616.5	17.9	1719	2	Q2Q3U4_DROYA	Q2q3u4 drosophila	RA Provost P., Samuelsson B., Radmark O.;
43	612	17.8	1719	2	Q2Q3U1_DROYA	Q2q3u1 drosophila	RT "Interaction of 5-lipoxygenase with cellular proteins.";
44	612	17.8	1719	2	Q2Q3U5_DROYA	Q2q3u5 drosophila	RL Proc. Natl. Acad. Sci. U.S.A. 96:1881-1885(1999).
45	612	17.8	1719	2	Q2Q3U3_DROYA	Q2q3u3 drosophila	RN [6]

ALIGNMENTS

RESULT 1	DICER_HUMAN	Reviewed; 1912 AA.					
ID	DICER_HUMAN	Reviewed; 1912 AA.					
AC	Q9UYF3; Q95943; Q8UQ02;						
DT	25-OCT-2002, integrated into UniProtKB/Swiss-Prot.						
DT	25-OCT-2002, sequence version 2.						
DT	24-JUL-2007, entry version 61.						
DE	Endoribonuclease Dicer (EC 3.1.26.-) (Helicase with RNase motif) (Helicase-MOI).						
GN	Name=DICER1; Synonyms=DICER, HERNA, KIAA0928;						
OS	Home sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;						
OC	Catarrhini; Hominidae; Homo.						
OX	NCBI_TaxID=9606;						
RN	[1]						
RP	NUCLEOTIDE SEQUENCE [mRNA].						
RX	MEDLINE=20246304; PubMed=10786632; DOI=10.1016/S0167-4781(99)00221-3;						
RA	Matsuda S., Ichigotani Y., Okuda T., Irimura T., Nakatsugawa S.,						
RA	Hamaguchi M.;						
RT	"Molecular cloning and characterization of a novel human gene (HERNA) which encodes a putative RNA-helicase."						
CC	-!- FUNCTION: Involved in cleaving double-stranded RNA in the RNA interference (RNAi) pathway. It produces 21 to 23 bp dsRNAs (siRNAs) which target the selective destruction of homologous RNAs.						
CC	-!- SUBUNIT: Interacts with PIWI1.						
CC	-!- INTERACTION:						
CC	Q9UL18:EIF2C1; NbExp=2; IntAct=EBI-395506, EBI-527363;						
CC	Q9UKV8:EIF2C2; NbExp=1; IntAct=EBI-395506, EBI-528269;						

CC Q8CJG0:Eif2c2 (xeno); NbExp=2; IntAct=EBI-395506, EBI-528299;
 CC Q8TB15:PIWI1; NbExp=1; IntAct=EBI-395506, EBI-527417;
 CC Q15633:TARBP2; NbExp=4; IntAct=EBI-395506, EBI-978581;
 CC -!- SIMILARITY: Belongs to the helicase family.
 CC -!- SIMILARITY: Contains 1 DRBM (double-stranded RNA-binding) domain.
 CC -!- SIMILARITY: Contains 1 helicase ATP-binding domain.
 CC -!- SIMILARITY: Contains 1 helicase C-terminal domain.
 CC -!- SIMILARITY: Contains 1 PAZ domain.
 CC -!- SIMILARITY: Contains 2 RNase III domains.
 CC
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 CC
 DR EMBL; AB028449; BAA78691.1; ALT_INIT; mRNA.
 DR EMBL; AJ132261; CAB38857.2; -; mRNA.
 DR EMBL; AB023145; BAA76772.2; ALT_INIT; mRNA.
 DR UniGene; Hs.87889; -.
 DR HSSP; O67082; 1JFZ.
 DR IntAct; Q9UPY3; -.
 DR Ensembl; ENSG00000100697; Homo sapiens.
 DR KEGG; hsa:23405; -.
 DR HGNC; HGNC:17098; DICER1.
 DR HPA; HPA000694; -.
 DR MIM; 606241; gene.
 DR PharmGKB; PA38437; -.
 DR ArrayExpress; Q9UPY3; -.
 DR GermOnline; ENSG00000100697; Homo sapiens.
 DR GO; GO:0005622; C:intracellular; NAS:UniProtKB.
 DR GO; GO:0003725; F:double-stranded RNA binding; IDA:UniProtKB.
 DR GO; GO:0005515; F:protein binding; IPI:IntAct.
 DR GO; GO:0004525; F:ribonuclease III activity; IDA:UniProtKB.
 DR GO; GO:0030423; P:RNA interference, targeting of mRNA for des. . .;
 IEP:UniProtKB.
 DR InterPro; IPR014001; DEAD-like_N.
 DR InterPro; IPR011545; DEAD_DEAH_N.
 DR InterPro; IPR001159; Ds_RNA_bd.
 DR InterPro; IPR005034; DUF283.
 DR InterPro; IPR014021; Helic_SF1/SF2_ATP_bd.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR003100; PAZ.
 DR InterPro; IPR000999; RNase_III.
 DR Gene3D; G3DSA:1.10.1520.10; RNase_III; 2.
 DR Pfam; PF00270; DEAD; 1.
 DR Pfam; PF00035; dsrm; 1.
 DR Pfam; PF03368; DUF283; 1.
 DR Pfam; PF00271; Helicase_C; 1.
 DR Pfam; PF02170; PAZ; 1.
 DR Pfam; PF00636; Ribonuclease_3; 2.
 DR SMART; SM00487; DEXDc; 1.
 DR SMART; SM00358; DSRM; 1.
 DR SMART; SM00490; HELICC; 1.
 DR SMART; SM00535; RIBOc; 2.
 DR PROSITE; PS50137; DS_RBD; 1.
 DR PROSITE; PS51192; HELICASE_ATP_BIND_1; 1.
 DR PROSITE; PS51194; HELICASE_CTER; 1.
 DR PROSITE; PS50821; PAZ; 1.
 DR PROSITE; PS00517; RNASE_3_1; 1.
 DR PROSITE; PS50142; RNASE_3_2; 2.
 PE 1: Evidence at protein level;
 KW ATP-binding; Endonuclease; Helicase; Hydrolase; Nuclease;
 KW Nucleotide-binding; Phosphorylation; Repeat; RNA-binding;
 KW RNA-mediated gene silencing.
 FT CHAIN 1 1912 Endoribonuclease Dicer.
 FT /FTId=PRO_0000180470.
 FT DOMAIN 41 217 Helicase ATP-binding.
 FT DOMAIN 423 592 Helicase C-terminal.
 FT DOMAIN 881 1032 PAZ.
 FT DOMAIN 1266 1393 RNase III 1.
 FT DOMAIN 1656 1814 RNase III 2.
 FT DOMAIN 1839 1904 DRBM.
 FT NP_BIND 34 41 ATP (Potential).
 FT MOTIF 165 168 DECH box.
 FT MOD_RES 654 654 Phosphotyrosine.
 FT CONFLICT 65 80 VLLTKELSYQIRGDFS -> STLLKSCLYLDLGETSA
 (in Ref. 1).
 FT CONFLICT 179 179 I -> F (in Ref. 1).
 FT CONFLICT 185 185 N -> I (in Ref. 1).
 FT CONFLICT 204 204 C -> W (in Ref. 1).
 FT CONFLICT 208 208 E -> D (in Ref. 1).
 FT CONFLICT 213 213 I -> F (in Ref. 1).
 FT CONFLICT 383 384 QQ -> HS (in Ref. 1).
 FT CONFLICT 482 483 KQ -> NT (in Ref. 1).
 FT CONFLICT 599 599 D -> H (in Ref. 1).
 SQ SEQUENCE 1912 AA; 217628 MW; 996399DB4B074F21 CRC64;
 Query Match 100.0%; Score 3446; DB 1; Length 1912;
 Best Local Similarity 100.0%; Pred. No. 4.8e-229;
 Matches 654; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 QVLKGRMDSEQSPSIGYSSRTLGPNGLQLQALTLSNASDGFNLRLLEMGLDSFLKHAIT 60
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Db 1259 QVLKGRMDSEQSPSIGYSSRTLGPNGLQLQALTLSNASDGFNLRLLEMGLDSFLKHAIT 1318
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Qy 61 TYLFCTYPDAHEGRLSYMRSKKVSNCNLYRLGKKKGLPSRMVVSIFDPVVNLPPGYVN 120
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Db 1319 TYLFCTYPDAHEGRLSYMRSKKVSNCNLYRLGKKKGLPSRMVVSIFDPVVNLPPGYVN 1378
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Qy 121 QDKSNTDKWEKDEMTKDCMLANGKLDEDYEEDEEEEMLWRAPKEEADYEDDFLEYDQE 180
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Db 1379 QDKSNTDKWEKDEMTKDCMLANGKLDEDYEEDEEEEMLWRAPKEEADYEDDFLEYDQE 1438
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Qy 181 HIRFDNMLMGSGAFVKKISLSPFSTTD SAYEWKMPKKSSLGSMPFSSDFEDFDYSSWDA 240
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Db 1439 HIRFDNMLMGSGAFVKKISLSPFSTTD SAYEWKMPKKSSLGSMPFSSDFEDFDYSSWDA 1498
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Qy 241 MCYLDPSKAVEEDDFVVGFWNPSEENCGVTGKQSISYDLHTEQCIADKSIADCVEALLG 300
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Db 1499 MCYLDPSKAVEEDDFVVGFWNPSEENCGVTGKQSISYDLHTEQCIADKSIADCVEALLG 1558
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Qy 301 CYLTSCGERAAQLFLCSLGLKLPVIKRTDREKALCPTRNFNSQQQNLNVSCAAASVAS 360
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Db 1559 CYLTSCGERAAQLFLCSLGLKLPVIKRTDREKALCPTRNFNSQQQNLNVSCAAASVAS 1618
 |||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||||/|||
 Qy 361 SRSSVLKDSEYGCLKIPPRCMFDHPDADKTLNHLISGFENFEKKINYRFKNKAYLLQAF 420

||||||||||||||||||||||||||||||||||||||||||||
Db 1619 SRSVLDKSEYGLKIPPRCMFDHPDADKILNLISGFENFEKKINYRFKNKAYLLQAF 1678
Qy 421 HASHYHNTITDCYQRLEFLGDAILDYLITKHLYEDPRQHSPGVLTDLRSALVNNTIFASL 480
||||||||||||||||||||||||||||||||||||||||
Db 1679 HASHYHNTITDCYQRLEFLGDAILDYLITKHLYEDPRQHSPGVLTDLRSALVNNTIFASL 1738
Qy 481 AVKYDYHKYFKAVSPELFHVIDDFVQFQLEKNEQMGMDSLRSEDEEKEEDIEVPKAM 540
||||||||||||||||||||||||||||||||||||
Db 1739 AVKYDYHKYFKAVSPELFHVIDDFVQFQLEKNEQMGMDSLRSEDEEKEEDIEVPKAM 1798
Qy 541 GDIFESLAGAIYMDGMSLETWQVYYPMMRPLIEKFSAANVPRSPVRELLEMEPETAKFS 600
||||||||||||||||||||||||||||||||
Db 1799 GDIFESLAGAIYMDGMSLETWQVYYPMMRPLIEKFSAANVPRSPVRELLEMEPETAKFS 1858
Qy 601 PAERTYDGKVRVTVEVGKGKFKGVGRSYRIAKSAAARRALRSKANQPQVPNS 654
||||||||||||||||||||||||||||||||
Db 1859 PAERTYDGKVRVTVEVGKGKFKGVGRSYRIAKSAAARRALRSKANQPQVPNS 1912

RESULT 2

AOMQHO_CRIGR

ID AOMQHO_CRIGR Unreviewed; 1917 AA.
AC AOMQHO;
DT 12-DEC-2006, integrated into UniProtKB/TrEMBL.
DT 12-DEC-2006, sequence version 1.
DT 24-JUL-2007, entry version 5.
DE DICER.
OS Cricetulus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathii;
OC Muroidea; Cricetidae; Cricetinae; Cricetulus.
NCBI_TaxID=10029;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wallerstorfer D.;
RL Submitted (SEP-2006) to the EMBL/GenBank/DDBJ databases.
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CC -----
DR EMBL; EF031271; ABK28790.1; -; mRNA.
DR GO; GO:0005622; C:intracellular; IEA:InterPro.
DR GO; GO:0005524; F:ATP binding; IEA:InterPro.
DR GO; GO:0003725; F:double-stranded RNA binding; IEA:InterPro.
DR GO; GO:0004386; F:helicase activity; IEA:InterPro.
DR GO; GO:0004525; F:ribonuclease III activity; IEA:InterPro.
DR GO; GO:0006396; P:RNA processing; IEA:InterPro.
DR InterPro; IPR014001; DEAD-like_N.
DR InterPro; IPR011545; DEAD/DEAH_N.
DR InterPro; IPR001159; Ds_RNA_bd.
DR InterPro; IPR005034; DUF283.
DR InterPro; IPR014021; Helic_SF1/SF2_ATP_bd.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR003100; PAZ.
DR InterPro; IPR000999; RNase_III.
DR Gene3D; G3DSA:1.10.1520.10; RNase_III; 2.